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EXECUTIVE MEETING OF THE INTERNATIONAL COMMITTEE  
ON TAXONOMY OF VIRUSES

AD-A246 824



FINAL REPORT

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DECEMBER 1, 1991

Supported by

U.S. ARMY MEDICAL RESEARCH AND DEVELOPMENT COMMAND  
Fort Detrick, Frederick, Maryland 21702-5012

GRANT No. DAMD17-91-Z-1024

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Center for Infectious Diseases  
Virology Division  
Atlanta, Georgia 30333

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# REPORT DOCUMENTATION PAGE

OMB No. 0704-0188

Public reporting burden for this collection of information is estimated to average 1 hour per response, including the time for reviewing instructions, searching existing data sources, gathering and maintaining the data needed, and completing and reviewing the collection of information. Send comments regarding this burden estimate or any other aspect of this collection of information, including suggestions for reducing this burden to Washington Headquarters Services, Directorate for Information Operations and Reports, 1215 Jefferson Davis Highway, Suite 1204, Arlington, VA 22202-4302, and to the Office of Management and Budget, Paperwork Reduction Project (0704-0188), Washington, DC 20503.

1. AGENCY USE ONLY (Leave blank)		2. REPORT DATE December 1, 1991		3. REPORT TYPE AND DATES COVERED Final 8 Apr 91 - 30 Sep 91	
4. TITLE AND SUBTITLE Executive Meeting of the International Committee on Taxonomy of Viruses				5. FUNDING NUMBERS DAMD17-91-Z-1024	
6. AUTHOR(S) Roger N. Beachy					
7. PERFORMING ORGANIZATION NAME(S) AND ADDRESS(ES) Center for Infectious Diseases Virology Division Atlanta, Georgia 30333				8. PERFORMING ORGANIZATION REPORT NUMBER	
9. SPONSORING / MONITORING AGENCY NAME(S) AND ADDRESS(ES) U.S. Army Medical Research & Development Command Fort Detrick Frederick, Maryland 21702-5012				10. SPONSORING / MONITORING AGENCY REPORT NUMBER	
11. SUPPLEMENTARY NOTES					
12a. DISTRIBUTION / AVAILABILITY STATEMENT Approved for public release; distribution unlimited				12b. DISTRIBUTION CODE	
13. ABSTRACT (Maximum 200 words)					
14. SUBJECT TERMS				15. NUMBER OF PAGES	
				16. PRICE CODE	
17. SECURITY CLASSIFICATION OF REPORT Unclassified		18. SECURITY CLASSIFICATION OF THIS PAGE Unclassified		19. SECURITY CLASSIFICATION OF ABSTRACT	
20. LIMITATION OF ABSTRACT					

NSN 7540-01-280-5500

Standard Form 298 (Rev. 2-89)  
Prescribed by ANSI Std. Z39-18  
298-102

THE 20TH MEETING OF THE EXECUTIVE COMMITTEE OF THE  
INTERNATIONAL COMMITTEE ON TAXONOMY OF VIRUSES: Virus  
Species, Higher Taxa, a Universal Virus Database, and  
other matters.

The Executive Committee of the International Committee on Taxonomy of Viruses (ICTV), comprising four office-bearers, six Sub-committee chairmen and eight other members, normally meets once in the interval between Virology Congresses to consider taxonomic proposals coming from 39 Study Groups covering the whole of virology, and to prepare these proposals for presentation to the full ICTV which assembles every three years concurrently with the International Virology Congresses. The 20th meeting of the Executive Committee of the ICTV was held at the Centers for Disease Control, Atlanta, Georgia, USA from 22nd to 24th April 1991. This meeting differed from the normal pattern of mid-term meetings in that it was convened for the specific purpose of considering in depth some of the broader aspects of viral taxonomy, and several co-opted guest speakers were invited to lead the discussion. The topics discussed were "The Issue of Higher Taxa", "The Species Concept in Virology", and "The Establishment of a Universal Virus Database". These topics will be the subject of more detailed articles in subsequent editions of Virology Division News, and only a brief summary of the proceedings is presented here.

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Perhaps the most significant outcome of the meeting was the acceptance of virus species as an entity in virus taxonomy, and the adoption of a new definition of virus species put forward by Marc Van Regenmortel.

Definitions of virus species based on biological (gene pools), ecological (niches), evolutionary (lineages), or phenetic (morphology) criteria were considered and rejected. The concept of the polythetic species, on the other hand, found general favour since it can accommodate the inherent variability of viruses and it does not depend on the existence of a unique diagnostic feature.

A polythetic class is distinguished from an ordinary class in that members of the former need not have any single property in common. Each member of a polythetic class is defined by more than one property, and no single property is necessary or sufficient for membership of a polythetic class. The strength of the polythetic species concept is that it does not depend on strict definition of boundaries, and the following definition of virus species was adopted: "*A virus species is a polythetic class of viruses that constitutes a replicating lineage and occupies a particular ecological niche*". The chairmen of the Sub-committees now have the responsibility of implementing this decision with the assistance of a guidance document from the Executive Committee, and of coordinating the activities of their Study Groups in this task. The chairmen of the Study Groups will be required to produce working definitions



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for delineation of species within existing families or virus groups, and to establish the criteria for differentiating species and strains. The polythetic species concept implies that there can be no common rules; the members of each Study Group must decide what is relevant to their group of viruses and devise diagnostic criteria accordingly.

The issue of higher taxa proved to be more contentious, and a consensus opinion was not obtained. As a consequence this matter has been deferred for further discussion at the next Executive Committee meeting. Anyone with views to air should approach either of the designated speakers, D.J. McGeoch and J.H. Strauss. The acceptance of the Order *Mononegavirales* as a taxon in virology at the last ICTV meeting in Berlin in August 1990 had created a precedent. Although it was agreed that the creation of the Order *Mononegavirales* fulfilled a useful function in gathering together three families of negative strand RNA viruses with related genome organisation, the opportunity to construct higher taxa is limited. For example, the remainder of the negative stranded RNA viruses which possess segmented genomes, on present evidence appear not be closely related to one another and cannot be included in a single order. Some of the factors which at present prevent the construction of hierarchies are the occurrence of recombination between viruses, the assimilation of host genes, the possibility of convergent evolution and the

homologies now recognised to exist between vertebrate and plant viruses. Nonetheless it was agreed that there are good operational reasons for establishing local hierarchies and that discussion of the issue should continue.

The greater part of the meeting was devoted to discussion of the establishment of a Universal Virus Database, and it was resolved that the ICTV should take the lead in coordinating efforts in this area and play an active role in the development of the most appropriate system. Marian Horzinek reported the results of a survey of current activity in this field carried out on behalf of the ICTV. Dr. Micah Krichevsky (NIH) presented a wide ranging appraisal of the technical aspects of database production and operation in microbiology, and Dr. Lois Blaine (ATCC) reviewed the requirements for a Virus Database and her work in compiling descriptors for use in a Virus Database. A low cost user-friendly system for vertebrate viruses using Superbase 4 software, which is at an advanced stage of development was demonstrated by A.J. Della Porta, and A.J. Gibbs described the powerful Delta-based system now being utilised as a research tool in plant virus taxonomy. The Executive Committee concluded that the problems in compiling a virus database were organisational rather than conceptual and the Data Subcommittee under Adrian Gibbs was delegated to carry the

matter forward with the aim of merging the two existing systems and developing a multi-purpose universal system.

The meeting also reviewed plans for preparation of the Sixth Report of the ICTV which is targeted for publication soon after the Ninth International Congress of Virology to be held in Glasgow, Scotland in August 1993. Publication of the much delayed Fifth Report, which will contain all the revisions of virus taxonomy which have accumulated since publication of the Fourth Report in 1982, is now scheduled for mid-summer 1991. The Fifth Report will be dedicated to the memory of Richard Francki, the past president of the ICTV, who was responsible for the final assembly of the Report and was undertaking the final revision at the time of his death in November 1990.

C. R. Pringle  
Secretary,  
ICTV.

(Corrected Minutes - 17th July 1991)

**MINUTES OF THE 20TH MEETING (MIDTERM) OF THE EXECUTIVE COMMITTEE  
OF THE ICTV HELD IN ATLANTA AT THE CDC, 22ND TO 24TH APRIL 1991**

**Members present:** F.A. Murphy (President)  
C. Fauquet (First Secretary)  
C.R. Pringle (Second Secretary)  
H.W. Ackermann  
P. Alquist  
L. Berthiaume  
C.H. Calisher  
S.A. Ghabrial  
A.J. Gibbs  
R. Goldbach  
A.W. Jarvis  
J. Maniloff  
G.P. Martelli  
M.A. Mayo  
M.D. Summers

**Guests:** A.J. Della Porta  
M.C. Horzinek  
B.W.J. Mahy  
D.J. McGeoch  
H.G. Pereira  
J.H. Strauss  
M.H.V. Van Regenmortel

**Observers for Database Session:**  
L. Blaine  
M. I. Krichevsky

**Apologies for absence:**  
D.H.L. Bishop  
F. Brown  
K.W. Buck (Vice-President)  
G.F. Rorhmann

**EC20/1 - Introductory Business**

In his role as Director of the Center for Infectious Diseases FAM welcomed Committee members and guests to CDC. He announced that this meeting of the ICTV would be dedicated to the memory of the Past President Richard Francki. Richard Francki had done yeoman service for the ICTV and the Fifth Report now nearing completion was largely the product of his sustained endeavour over the past three years. The Fifth Report was almost ready for publication and it would be dedicated to the memory of Richard.

The President introduced his secretary, Diana Yancey, who would be providing secretarial support for the meeting.

Dr. Brian Mahy as Director of the Division of Viral and Rickettsial Diseases welcomed participants to CDC, and as Chairman of the Virology Division of IUMS expressed his hope that the meeting would be productive. The ICTV was the only Committee supported by the Virology Division, and the parent body was concerned to promote its success. He summarised briefly the outcome of the IUMS meeting in Berlin and reminded participants that the next Virology Congress would be held in Glasgow in August 1993. It was intended on this occasion to arrange a more balanced programme covering all aspects of virology. Intervirology and Karger had relinquished their association with the Virology Division of IUMS, and the Archives of Virology was now the official journal of the Virology Division. A regular section devoted to Virology Division news, including ICTV business, was now being edited by MCH; it was hoped that this venture would yield regular revenue, some of which would be used to support ICTV activities.



FAM then outlined the goals and objectives of the midterm meeting and the Agenda was finalised. There would be four sessions spread over the first two days; Session 1 devoted to regular ICTV business (chaired by FAM and CF), Session 2 concerned with the issue of higher taxa (chaired by DJM and JHS), Session 3 dealing with the concept of virus species (chaired by MHVR and MDS in the morning and HWA and GPM in the afternoon), Session 4 considering symmetry (or parallelism) between taxa in different families (chaired by BWJM and JM). The whole of the final day was allotted to Session 5 which would be devoted to consideration of the design and establishment of a virology database (chaired by AJDP, AJG and MCH in the morning and CHC and CRP in the afternoon). ICTV must play a leading role in development of a virology database, and it would be essential to produce a plan of action by the end of the meeting. ICTV had in the past neglected this area and by default other organisations were stepping in. ICTV must act immediately to regain the initiative in this area. L. Blaine (ATCC), R. Robbins (NSF) and A. Schluderberg (NIAID, NIH) had been invited to attend Session 5 to provide advice and information of database development.

CF described the fund-raising effort which had been necessary to provide financial support for the midterm meeting. Substantial contributions had been received from IUMS, NIH, NSF, EEC, ASM, FEMS and CDC, and smaller amounts from elsewhere. Some of these agencies could not be approached a second time and suggestions for other sources of support for the second midterm meeting would be welcome. Fund-raising initiatives would be coordinated by CF. It had been found that in general sponsors were interested more in the database proposals than virus taxonomy. The document prepared for approaches to potential sponsors would be amended to take this into account.

EC20/2 - Session 1 (Part 1) - Regular ICTV Business -  
(Monday a.m.)

- FAM - The final preparation of the Fifth Report had been taken over by CF following the untimely death of Richard Francki. There had been both formatting and unresolved taxonomic problems, but the final draft document was now in the hands of Springer Verlag. The report was seven years late. Imperfections remained partly because three separate teams had been involved. Some 2,400 viruses were listed in approximately 450 pages and it was hoped that the publication target of July would be achieved.
  - CHC - Cost and distribution to the Executive Committee?
  - FAM - Each member of the Executive Committee would receive a copy. It would be marketed at \$60 a copy.
  - MCH - Are royalties payable?
  - MHVR - Royalties would be paid at the rate of 5% from the first copy (whereas royalties on journal sales were not payable on the first 700 copies).
  - MCH - The copyright goes to Springer. In future the ICTV should retain the copyright.
  - FAM - This would be arranged in future.
- CF had worked very hard on behalf of ICTV to get the final document ready for publication, and deserves our thanks. A saving of 20% in cost had been achieved by providing camera-ready material. This has the added advantage of indicating that the ICTV Report is a publication under regular revision.
- CF - Many problems remain unresolved and will have to be considered in preparing the Sixth Report in order to achieve greater uniformity. For example, currently there is a lack of uniformity of treatment (1 - 15 pages of description) and referencing (1 - 47 items). There is the question of the ranking of the plant virus groups - genera or families? Richard Francki considered that they should be ranked as families. Should we amend this? Another problem is authorship; the London meeting suggested all descriptions should be attributed to Study Groups, but the revised descriptions in the Fifth Report will be attributed to Study Group Chairmen only.
  - MHVR - Some comments on the family/genus problem. There are a large number of monogeneric families, consequently the ability to form sub-divisions is lost. The decision to equate groups with families appears has been taken without consultation. We need definitions of the names - family and genus - so that this confusion does not arise. The Plant Virus Sub-committee has decided that these groups can be equated with genera, which will give scope for reducing the number of families.

- CF - It would be possible but inconvenient to alter the text at this late stage. The Fifth Report is a reflection of the decisions of the Plant Virus Sub-committee.
- GPM - The Plant Virus Sub-committee only accepted the need to rename groups as genera after the Berlin Congress, following circulation of a questionnaire to which most members responded. A list of possible families is on the table at this meeting. There is agreement on designation of the families *Rhabdoviridae* (with two genera), *Bunyaviridae*, *Reoviridae*, *Cryptoviridae* (with two genera), *Geminiviridae* (with three genera), and *Caulimoviridae*. The *Badnaviridae* is another possible family, but the name is in dispute; it was rejected in Berlin, but it remains a generally accepted designation. For the time being all the others must be considered undecided categories until more information becomes available to assign them as genera or families. It is hoped that firm proposals will be ready by the next meeting.
- FAM - We must complete the pyramid even if all the parts are not named, i.e. there must be no free-flowing categories. Rule 22 says that approval of a new family must be linked to approval of a type genus.
- CF - Unfortunately, anomalies already exist. Some families have no genera.
- LB/AG - Is there any real need to complete the pyramid at this stage?
- GPM - The "undetermined taxon" is the device employed to avoid this confrontation
- FAM - There are two views: either press ahead and make decisions now (in fact the animal virus families have been designated on the basis of very modest information), or defer decisions to the Sixth Report.
- MHVR - This is a major problem; the disputed groups comprise half the Report. There will be an adverse reaction to the Report if changes are not made, particularly as the Fourth Report appeared 9 years ago. I propose that "the Summary Tables in the Fifth Report be changed to read Genus/Group instead of Family/Group". (EC20/2/1).
- FAM - This proposal is now adopted.
- CF - The Bacterial Virus Sub-committee must also bring their descriptions into line. "Type member" should be changed to "Type species". To minimise such problems in the future, a set of guidelines will be prepared by FAM and CF for distribution to Sub-committee and Study Group chairmen prior to revision of descriptions for the Sixth Report. (EC20/2/2). It is the future intention to produce a Report triennially to appear immediately after each Virology congress.
- FAM - It will be necessary to arrange a second midterm meeting, perhaps in conjunction with an ASV or SGM meeting to reduce expenses. This will be the time to review new proposals for presentation to the ICTV at the 9th Congress of Virology in Glasgow. The aim will be to publish the Sixth Report containing the newly approved proposals within three months. Sub-committee Chairmen should circulate the guidelines and template to Study Group Chairmen as soon as they become available. (EC20/2/3). A draft copy of the Fifth Report is on the table for inspection.
- LB/AG - The line diagrams need complete revision. Some represent EM cross-sections, others EM negative stained images, and some are cartoons.
- FAM - The collective term is artistic licence. The diagrams need improvement, rethinking and augmentation. However, the final preparation should be handled by a single individual to obtain uniform graphical representation.
- JM - As teaching aids they are invaluable. They should certainly be improved but on no account omitted.
- FAM - This matter will be considered by a Sub-committee comprising HWA, CHC, LB (Chairman), and RG. (EC20/2/4).
- DJM - There is too much information available to be reduced to a single diagram. Another problem is the differences in scale. It is appropriate now to move to a more comprehensive system of representation.
- JM - Provision of genome diagrams and database accession numbers would be useful. The relevant information should be compiled by Study Groups and Sub-committees.
- FAM - Regarding the question of authorship, a broad credit is the best solution. The listing of entire Study Groups as authors is unnecessary, since the Study Groups will be listed separately at the front.
- MDS - Where the revision is attributed to the whole Study Group, it would be sufficient to say "revised by the Study Group".

The question of denoting authorship was put to a vote, and the majority favoured a compromise solution to be left to the discretion of the President. Subsequently following an intervention by DHLB and in line with a decision at a previous meeting the President decided that from the Sixth Report onwards all members of Study Groups would be listed as authors of family descriptions. (EC20/2/5).

- CF - A uniform system of referencing is desirable, perhaps citing general references only.
- JM - The references should be recent and sufficient only to provide a starting point.
- CF - The template to be provided for Chairmen will stipulate a limit, probably a single page (i.e. about 20 references).  
Another problem to be considered is the listing of member viruses. Should Possible Members and Probable Members be listed also?
- MDS - In many cases this will not be feasible; e.g. there are more than 600 baculoviruses. It should be the responsibility of the Chairman to compile the list and decide status without recourse to use of references.
- FAM - Double column printing could be adopted to accommodate large numbers, with elimination of synonyms. The designations Member/Probable Member/Possible Member will have to be retained; some Study Groups insist on this.
- MHVR - A list of acronyms for plant viruses (compiled by Milne, Hull and Van Regenmortel) has been approved and will appear in Archives of Virology. This will not appear in the Report, because it was not discussed by the Executive Committee. Perhaps there is a need for lists of acronyms for other groups? A universal acronym list for all viruses is not practical and is not necessary.
- FAM - It is too late now to prepare an exclusive list; e.g. CMV is in common useage for both cytomegalovirus and cucumber mosaic virus. Perhaps an approved acronym could be included after the virus name in the next Report?
- DJM - Acronyms are used for local convenience and they are not open to systematisation. ICTV should not attempt to impose acronyms, although it would be reasonable to prepare lists of preferred acronyms.

The matter was put to a vote. There was a majority for the proposition that acronyms in common useage should be included in the Sixth Report. DHLB in his absence was delegated to prepare a list of acronyms of vertebrate viruses. (EC20/2/6).

A proposal to adopt badnavirus as a group name was also carried without dissension. (EC20/2/7).

#### Session 1 (Part 2)- ICTV Regular Business - Subcommittee and Study Group Business (Tuesday a.m.).

- FAM - It has been proposed that all members of Study Groups should be made members of the ICTV. This would mean addition of some 300 names and an inherent imbalance in the ICTV since c. 250 are vertebrate virologists.
- DJM - What regulates the number of Study Groups and the number of members?
- FAM - There are no rules.

It was decided that since Study Group members are listed in the ICTV Reports, they receive adequate recognition and they should not be given voting rights.

- MDS - Invertebrate Virus Sub-committee business: (1) A query from R.Ruekart (Picornavirus Study Group) regarding the *Nodaviridae* and the *Tetraviridae*; whose territory? A major task of the Iridovirus Study Group is to address the taxonomic position of African swine fever virus.
- FAM - The insect picornaviruses should be the responsibility of the Picornavirus Study Group, provided the Group includes insect virologists.
- GPM - Plant Virus Sub-committee business. The Potyvirus Study Group will propose the formation of the family *Potyviridae*. Two new Study Groups are proposed: one under Milne to consider the elongated plant viruses together with the potex and carla virus groups, the other under Morris to consider the tombus and carmo virus groups.

- AWJ - Bacterial Virus Sub-committee business. Thirteen Study Groups are active; some will be reorganised, no new ones are proposed. HWA and the Bacterial Virus Sub-committee are preparing a paper on the species concept in bacterial virology. Schneider and the Bacterial Virus Sub-committee are preparing a paper describing DNA homology as a criterion for classification.
- SAG - Fungal Virus Sub-committee business. A description of current and planned projects was placed on the table. A problem to be resolved is the position of the group of naked viral-like dsRNA genetic elements.
- MDS - Perhaps this should not be considered until some sequence information is available.
- MAM - In the case of the umbraviruses, another group with indeterminate genetic properties, a decision was deferred on the grounds that they might turn out to be defective viruses of a known virus.
- FAM - The Fungal Virus Study groups should maintain a watching brief. It is part of the responsibility of ICTV to define viruses; e.g. the ICTV should be considering the spongiform encephalopathy agents.
- AJG - Code and Data Sub-committee business. A survey of current attempts to devise virus databases has been compiled by MCH. These matters will be discussed in detail in Session 5. Lois Blaine (ATCC) has been devising a set of descriptors, and she has been invited to join the Sub-committee. Dr. Dalwitz has also been invited to join the Sub-committee.
- FAM - Finally we should consider whether any new Study Groups are required.

Going round the table, the following were suggested: the Circoviruses; the Astroviruses; the Ascoviruses; the Picobirna viruses - the name proposed for the small enteric dsRNA viruses being characterised by HGP that are most similar to the cryptoviruses of plants, despite the occurrence of 3 and 5 segmented genome viruses.

- FAM - DHLB will be asked to maintain a watching brief for the vertebrate viruses and to decide when and whether Study Groups are required. In general it should be the function of Subcommittee chairmen to maintain surveillance in their areas. The Fifth Report contains nothing on unclassified viruses. Should they be mentioned in some way?
- MDS - Each Sub-committee chairman should be asked to compile a list of unclassified agents with references. Unpublished information should not be used.

**It was agreed that each Sub-committee chairman should prepare a list of unclassified agents for consideration at the next meeting. (EC20/2/8).**

- AJG - In the case of plant viruses this may produce a list of some 500 names.
- MHVR - Only those unclassified viruses should be listed which have been studied sufficiently to ensure that they are distinct from known viruses.
- FAM - How should viroids and satellites be handled?
- GPM - This is under consideration by the Plant Virus Study Group.
- FAM - MAM has been delegated to represent the ICTV at a satellite meeting on the island of Rhodes.

**It was decided that MAM should set up an ad hoc Study Group on satellites. (EC20/2/9).**

- AWJ - Three proposals are on the table (see Appendix 1).
- CF - According to the Rules these should have been circulated prior to the meeting. It would be appropriate to consider these three proposals at the meeting next summer.
- GPM - There is a proposal to establish Idacovirus as a possible genus (Appendix 2).

It was decided that these proposals should all be considered on the third day of the meeting.

## EC20/3 - Session 2 - The Issue of Higher Taxa

- FAM - The principal reason for convening this midterm meeting is to promote discussion of some of the more general aspects of virus taxonomy and to frame proposals if possible. The only fixed point at present is the recently approved Order *Mononegavirales*. One device to avoid the nomenclature trap, however, would be like Woese to rely only on vernacular terms. JHS and DJM will now open the Discussion.
- JHS - Higher taxa should reflect evolutionary relationships (phylogeny). Strains can be grouped with a fair degree of confidence, but above this level it becomes problematic. Coherent trees are difficult to construct because of the prevalence of recombination. It does not make sense to take a single gene (e.g. RNA polymerase) and to group all viruses that share homology in one order. Some viruses exchange genes and even acquire genes from their host; for instance the three dimensional structure of the Sindbis virus capsid protein is similar to that of chymotrypsin.
- DJM - Opportunity to construct higher taxa is only sporadic and limited. The creation of the Order *Mononegavirales* to embrace the non-segmented negative strand viruses is probably justified, as might be an order to include the segmented genome negative strand viruses, and there may be other coherent groups such as the plus strand RNA viruses. However recombination and the homologies between animal and plant viruses pose problems in establishing any hierarchical structure. A classification based on genome structure is not possible; the herpesviruses illustrate the dilemma. Channel catfish virus has a genome structure with similarities to other herpesviruses, but it is totally unrelated in terms of nucleotide sequence. Similarly how do we evaluate the resemblance of parvovirus capsid protein to the capsid proteins of RNA viruses. A hierarchical classification has sets of branch points, but from our standpoint we have no means of discriminating branch points from separate origins. The Order *Mononegavirales* is reasonable since it is a product of experimental research. However, the ICTV should not seek to impose a classification in the absence of research.
- MHVR - I do not believe that phylogeny will help at the order level. Proteins consist of assemblies of domains. The number of domains is limited because the number of conformational arrangements is restricted. As a consequence proteins cannot be used to define taxonomic relationships at higher levels, since different proteins may be produced by shuffling domains (e.g. such a process provides an explanation for the occurrence of a protein with epidermal growth factor activity in vaccinia virus). Genome properties (type of nucleic acid, segmentation, strandedness) and morphology provide better opportunities for establishing a hierarchical classification.
- PA - It is also a question of purpose. I agree with the remarks of JHS: It is presently difficult to envision how to properly define higher order taxa because this would require selecting a single criterion over others for defining the branch points. The real phylogeny of viruses is more complex and involves recombinational gene reassortments. However much we would like to make higher order groupings now, we should not institute any oversimplified schemes based on the arbitrary emphasis of one or a few criteria over others. Regardless of whether such oversimplified schemes are based on a single gene sequence or on morphological characters, they would not reflect the complex nature of the true phylogeny.
- BWJM - The replicative strategy is the critical element and has been a stimulus for developing new ideas about relationships.
- AJG - I still favour the development of hierarchies based on phylogeny as far as possible. Virus evolution differs from that seen in other organisms. Hierarchies should be built up locally without any requirement for linking into a tree-like structure. There is no need to apologise for the lack of a unique hierarchical structure.
- RG - Designation of the unsegmented negative strand RNA viruses as an order is a bad precedent. *Mononegavirales* is an unfortunate choice of name, since it implies the existence of a corresponding group the Multinegavirales. Segmentation of the genome is not a suitable property for differentiating higher taxa. The study of polymerase sequence relationships (data presented as slides) suggests that the orthomyxoviruses on the one hand are quite distinct from the arenaviruses and the

bunyaviruses on the other. To accommodate these differences it would be necessary to create two new orders. Perhaps the Order *Mononegavirales* should rank as a family with corresponding down-grading of its constituents. The same rate of divergence (even including splitting of the genome) is found within the newly established family of *Potyviridae*.

- MHVR - Perhaps Super-family would be preferable to Order.
- CRP - The rationale for establishing the Order *Mononegavirales* to embrace the existing families, *Filoviridae*, *Paramyxoviridae* and *Rhabdoviridae* is summarised in the article printed in the second issue of Virology Division News (in Archives of Virology 117, 137-140, 1991). The Paramyxovirus Study Group considered that there were five clear categories to be accommodated in any system of classification (i.e. [species], genera, sub-families, families and a super-family or order). By long usage the families were considered fixed points. The Study group preferred the introduction of a new taxon, the order, rather than qualification of an existing category that might imply degree of relationship or direction of evolution. The use of the term sub-family is inconsistent with this argument, but was unavoidable. I agree that this may be something of a special case and not directly applicable to other groups of viruses.
- RG - Comparison of conserved regions of polymerase genes would be appropriate.
- AJG - A combination of morphological characteristics and polymerase sequence might be an approach to establishing a time dependent scale
- HWA - The discussion so far has focussed on small viruses with RNA genomes. It is difficult to make inferences about evolutionary origins in the case of the larger DNA viruses. In the case of DNA phages, converting phages have acquired genes from their hosts. The emphasis on polymerase genes is unwise, since it can only apply to RNA viruses.
- MAM - The introduction of the taxon order has been premature.
- JM - We should stop pushing towards definition of higher systems because of the diversity of the processes involved in virus evolution. Virus evolution is polyphyletic. We can only with confidence group species in genera. Because in one case it is possible to trace relationships back to the order level, it does not mean that this can be done universally. It is instructive to consider bacterial taxonomy. In the case of the eubacteria, a tree based on molecular data reveals mistakes which are the result of basing existing taxonomy on phenotypic characteristics. Some useful distinctions were made (e.g. Gram colouration), but other fundamental characteristics (e.g. photosynthesis) were ignored.
- FAM - Taxonomy emphasizes similarities, whereas molecular approaches emphasize differences. If the emphasis is put on difference, all viruses are different from one another, the more so the larger they are. I perceive too much respect for words, and an unwillingness to use new terms such as super-family and order.
- AJG - This is precisely the reason why plant virus classification is out-of-step.
- LB - We must surely attempt to define categories.
- JM - Woese only worked at two levels; species and kingdoms.
- FAM - We can set up strawmen for the sake of discussion. For example, rather than forcing togetherness, perhaps we should consider raising the families *Poxviridae* and *Herpesviridae* to the rank of Orders because of their lack of relationship with other groups?
- MHVR - If segmentation is not suitable for designating an order, we must consider whether we want to use molecular or old-fashioned criteria. I would be more confident about a classification based on morphology rather than one based on a single gene.
- AJG - In some situations morphology may only reflect a single gene difference.
- RG - The single gene approach has inherent problems. If the polymerase gene comparisons discussed previously are taken as an example, a different classification would have been arrived at if possession of helicase activity had been used as a diagnostic property.
- DJM - Convergent evolution is likely in viruses with their high mutation rates.
- AJG - The polymerases may not have such great variability because they are associated with stable genes.
- MAM - The criteria must reflect what we know now; the amount of sequence information is not great.

- RG - This is not so; genome sequences have been determined for viruses belonging to most of the major groups.
- HWA - This does not apply in the case of the phages. About 3,000 distinct tailed phages are recognised, but only lambda and three others have been sequenced in the last 9 years.
- MAM - CF and I have attempted to produce an identification key for families and groups (Appendix 3). The interesting result is that like tends to end up close to like.
- FAM - This pragmatic approach might define clusters and circumvent the problem of phylogeny.
- PA - One purpose of virus taxonomy is to simplify recall, stimulate research, etc. Whatever we decide should provide something for the user.
- HWA - If there is a requirement for orders in some fields, what is wrong with having different criteria according to group? Define the order where it is possible and forget the others rather than strive to achieve the impossible
- FAM - I do not think we can achieve a consensus opinion on higher taxa as the result of these discussions. I propose that we delegate JHS and DJM to reflect further on this problem and to present their further conclusions for continued discussion at the next meeting of ICTV. (EC20/3/1).
- MHVR - Earlier we agreed that viruses are polyphyletic, therefore standardised criteria for higher categories are not required.
- AJG - I do not agree. Local phylogenies can be traced back so far. These should be merely listed alphabetically.
- RG - Up to the family level it may not be difficult to achieve a consensus opinion, but beyond that level it will be difficult.
- PA - To provoke wider discussion the President of ICTV should prepare an article for Archives of Virology summarizing the opposing views and emphasizing the polyphyletic concept.
- FAM - I am in agreement provided that the summary paper is intended to stimulate discussion and debate. The factual content should not be controversial. I propose that a position paper for Archives should be compiled by JHS, DJM, with contributions by KWB and FAM). (EC20/3/2). The question of the order of presentation of virus groups has to be considered for the Sixth Report. Currently the arrangement of groups is biased in favour of envelope characteristics. Should an identification key be included? Currently virology is taught from a taxonomic base; it is one of the responsibilities of ICTV to provide guidance.
- AJG - The animal and plant viruses were arranged in separate alphabetical order in the First and Second Reports of ICTV, and subsequently the Matthews' approach emphasizing envelope characteristics was adopted.
- CF - At the London meeting of ICTV the decision was made to retain the Matthews' system.
- HGP - This is the order adopted by most textbooks; it would be inadvisable to change.
- PA - Perhaps in the Sixth Report there should be a discussion of higher taxa, the polyphyletic approach, etc., as part of the President's Report or separately. The report should also include a consideration of the relationships of animal and plant viruses.
- MCH - Publication in the Sixth Report might be too definitive.
- MHVR - This is too difficult a task for a single person; the forum approach would be better.
- FAM - An alternative and more satisfactory approach would be to replace the President's Report with an Executive Committee Report. A longer version could be published in Archives of Virology. The following are delegated to consider this further: RG (Chairman), JHS, DJM and MHVR. (EC20/3/3).

#### EC20/4 - Session 3 - The Concept of Virus Species (Tuesday a.m.)

- MHVR - (I) Let us consider why the species concept is applicable to viruses. Viruses are biological entities not chemicals. Molecules are identical, viruses possess intrinsic variability. Viruses possess genomes and by mutation evolve to occupy niches. A distinction can be made between the species as an abstract concept and as a concrete object. In the abstract the species is a category which can be defined (e.g. element 79), whereas the species as a



taxon is a real object which can be named but not defined (e.g. a piece of gold)

(II) The definition of the species.

Based on concepts of reproductive isolation and gene pools (Mayr, 1963). Mayr (1982) accepted that such a definition could not accommodate clonally reproducing organisms, and produced a new definition - "reproductive community of populations, occupying a specific niche in nature" - which did not include sexuality. Neither sex nor genetic compatibility are essential to this definition. This definition was attacked because of the difficulty of defining niche.

Objections to reproductive isolation as a definition are that it is often an untested assumption, and where tested is found wanting; e.g. hybridisation in plant breeding, interbreeding of animals (dogs, wolves, jackals) considered to be species.

(III) Criteria for species.

Species are frequently defined on morphological criteria only, and the degree of morphological similarity is assumed to be proportional to evolutionary divergence.

The idea of the evolutionary species was introduced by Simpson (1961). At some point in the divergence of lineages, they become separate entities. There are no common criteria, however, and the idea has little practical value.

So far we have considered the phenetic (morphology), biological (gene pools), ecological (niches) and evolutionary (lineages) species concepts. Now let us consider the concept of the polythetic species (first introduced by Beckner in 1959). A polythetic class is distinguished from an ordinary class in that the members of the former need not have any single property in common. Each member of a polythetic class is defined by more than one property, and no single property is necessary or sufficient for membership of a polythetic class. This system of classification is appropriate in virology since it takes account of the inherent variability of individual viruses. The number of properties used can be very large. The advantage of the polythetic species concept is that it does not depend on definition of boundaries. A useful analogy is the perception of individual colours by the human mind from a continuous spectrum of electromagnetic radiation.

Several virus species definitions have been proposed by ICTV. In 1981 at Strasbourg the species was defined as a cluster of strains having a set of properties in common. At Sendai in 1985, Kingsbury proposed that the species be considered as a population of viruses with a common gene pool that is normally isolated from the gene pools of other viruses. A weakness of this definition is that not all viruses have gene pools. Finally in 1989 I proposed the species be considered as a polythetic class consisting of a replicating lineage occupying a particular ecological niche. Earlier Domingo had promoted the idea of the "quasispecies" representing a weighted average of a large number of individual genome sequences. To accommodate both ideas, it must be assumed that a "master" genome (species) is maintained by selection for survival in a particular niche.

For the Sixth Report we must now decide on a new definition of species to replace virus (which in any case has not been defined). Morphology, replication strategy and genome characteristics define families and genera, whereas genome characteristics, antigenicity, vectors and hosts define species. What are the properties of diagnostic importance? To some extent this must be left to Study Groups to decide. They should include morphology, genome characteristics, replication strategy, level of genome homology (sequence, reassortment, recombination, complementation), level of serological cross-reaction, host range, tropism, vectors *et al.* No single criterion can be used.

We should not at this stage attempt to define or include any categories (e.g. strains, members, etc) below the species level, although each Study Group should be asked to address this problem. To take the potyviruses as an example which include 50% of plant viruses. Extensive cross-reactivity



and sequence information is available for about 30% of potyviruses. There appears to be a discontinuity at 20% sequence difference which could be used to distinguish strains and species (<20% = strains, >20% = species; see Fig. 15, page 298, Adv. Virus Res. vol. 36).

- RG - How do we deal with hybrids? In some cases (e.g. tobnaviruses) these may be difficult to recognise.
- MHVR - Should be called species because they are the equivalent of new species.
- DJM - Is member the term to be used where information is lacking?
- MHVR - The question is member of what?
- GPM - Member of the genus.
- JM - There is a need to define strain and member.
- RG - In the case of plant and vertebrate viruses, member = species; whereas member = strain in bacterial viruses.
- HGP - The term member can be applied to any category, order, family, genus or species.
- FAM - We should strive to substitute species for virus wherever possible.
- MDS - If species is to replace virus, can we have probable and possible members of species?
- MCH - If we accept the hierarchy, member becomes redundant. Doubtful cases should be grouped as species and redefined as information accumulates.
- AWJ - The strain is the equivalent of possible member of species.
- MHRV - Variants are below strains, and strains are members of species. Species can only be members of higher-level categories.
- GPM - Nothing below the level of species should go into the ICTV Report.
- CF - There is a consensus for species; species will be included and anything else left until the next occasion.
- RG - What about the viroids?
- GPM - We should wait for the recommendation of the Study Group; as yet there is no classification.
- FAM - We must await proposals from the Study Group; Randles has a watching brief and responsibility to keep things moving.
- MHVR - Is the consensus that the term member should be abolished and strain used in its place?
- FAM - Let me sum up this discussion so far. This is a milestone in the activities of the ICTV. There has been conceptualisation of the species at this meeting. I propose that we vote on the following proposal: that the species concept as elaborated here this morning by MHVR be accepted by the ICTV. (EC20/4/1).

This proposal was accepted unanimously.

- AJG - An alternative proposal. "A virus species is a collection of isolates/strains that are so similar that it is useful to give them a single name". Or in more extended form "A group of viral isolates/strains that are (1) genetically similar as a result of common ancestry, and (2) share in particular the genetic information that is under stabilising selection".
- DJM - Such a definition does not include relationship to higher taxa.
- MDS - "Replicating lineage" covers all of the above and implies stabilising selection.
- MHVR - The first definition proposed is minimal. Polythetic is the key element. It avoids the error of looking for an elusive property that will define a single class.
- FAM - This is matter which must be resolved before we proceed to the discussion of databases.
- JM - If the first proposal is accepted, it should be followed by an explanation of polythetic class, replicating lineage, and ecological niche.
- MHVR - A definition of polythetic class is the following: "A class defined by a combination of unifying characters no one of which is necessary or sufficient to define the class".

After some discussion the alternative definition proposed by AJG incorporating the idea of stabilising selection was withdrawn and the first proposal was put to a vote. The proposal was approved by 14 votes for to one against. The definition approved for inclusion in the Sixth Report to replace rule 10 is that: "A virus species is a polythetic class of viruses that constitutes a replicating lineage and occupies a particular ecological niche". (EC20/4/2).

**It was further agreed that a sub-committee of CHC, JM and MHVR will prepare definitions of the terms polythetic class, replicative lineage and ecological niche, and report their decisions to ICTV within three months. (EC20/4/3).**

- FAM - The viruses listed by CMI and the Arbovirus catalogue should be considered species for the present.
- HWA - A working definition for the tailed phages would be that a species is a group of phages with greater than 70% genome similarity, but accepting the polythetic definition other characteristics need to be added.
- FAM - The type species needs to be redefined. Sub-committee chairmen should prepare an accepted list of species. Should the present format of the Report be continued, or should we move towards elimination of English vernacular names; e.g. the type species of human adenovirus is given as H2, which is a designation no longer in use. This is another point which Sub-committee chairmen should consider. In general "member" should be eliminated and "unassigned" retained to cover possible and probable species. **I propose that the Sub-committee chairmen should instruct Study Group Chairmen to delineate species, and the Executive Committee should formulate a guidance document within the next month. None of the properties need imply a hierarchy and Study Groups should not search for such. (EC20/4/4).**
- DJM - I am still unhappy about the omission of consideration of hierarchy. There has been no consideration of the nature of the characteristics which can or should be used.
- MHVR - The Study Groups should be given some freedom in this respect. A 1% genome difference has different importance in different circumstances, therefore genome similarity by itself is not meaningful.
- AWJ - How do we know whether to use 2 or 10 phenotypic characteristics?
- MHVR - There can be no rules. The amount of change required to discriminate species is not uniform.
- FAM - In practice how do we achieve this? The Executive Committee of ICTV does not want to be concerned with anything below species level.
- MHVR - The Study Groups must establish their own diagnostic criteria; they must be left to decide what is relevant in specific circumstances. A blanket set of rules is not attainable.
- MAM - Every genus has a description, therefore every species will need a description.
- HGP - Let us consider an example. Bipartite genome double-stranded RNA viruses have been isolated from mammals, and therefore differ in host range from previously known birnaviruses. They have other distinctive properties and they appear to represent a new group. How are these agents fitted into the system?
- FAM - In the past there have been two routes used: Some have published data and proposed creation of a new family, presenting ICTV with a *fait accompli*; others have first approached ICTV directly.
- HGP - We should also give some thought to how useful the Report is to the user.
- GPM - The ICTV Report is useful at the family and genus level, but in its present form it is not useful at the species level.
- MCH - There are instances where it is difficult at present to determine taxonomic status. For example, Berne virus of horses has a genome structure like coronaviruses, but it has other distinguishing properties. Should it be ranked as new a species, genus or a new family - the *Toroviridae*? It is impossible to decide as there is only one representative so far.
- FAM - In bacteriology a new family would be created, but many veterinary virologists would prefer to leave Berne virus unassigned for the present.
- MCH - A contrasting example is equine arteritis virus which is considered to be a togavirus at present. But it has genome characteristics intermediate between togaviruses and coronaviruses. Should a new family be created?
- FAM - It should be left unassigned or placed in a monospecific taxon and redefined later.
- JHS - There are parallels in other organisms; some avian orders are represented by single species. We cannot logically take a stand against monospecific taxa.
- FAM - It would be reasonable to consider order status for the positive strand RNA viruses synthesising a nested set subgenomic mRNAs. Let us consider another

- point. What is the current opinion on the old idea of Fenner/Matthews/Gibbs of incorporating the genus name into the designation; e.g. rabies lyssavirus.
- GPM/ - This is preferable provided the acronym is unaffected; e.g. tobacco mosaic
  - MAM/MVR - tobamovirus would still be TMV.
  - MCH - It is useful for the reader; e.g. mouse hepatitis coronavirus is more instructive than mouse hepatitis virus.
  - AWJ - Most bacterial viruses do not have genus names.
  - FAM - I think consideration of this matter should be deferred to the next meeting, and I propose that it should form part of the Agenda in the form of a substantial proposal with examples. (AJG and HGP were delegated to prepare a background proposal for the next meeting). (EC20/4/5).
  - FAM - The next session was intended to consider the topic of Symmetry and Parallelism, but I do not think we can have any fruitful discussion without knowledge of how Study Groups operate and reach their decisions. I propose that JM should frame a letter to Sub-committee and Study Group chairmen requesting information on this point, and the results of this survey circulated to all Executive committee members. (EC20/4/6). An example of how a specific proposal has been prepared would be instructive. It would also be useful to include in the letter a request for other comments. This would give Study Group Chairmen an opportunity to voice complaints and make suggestions; in turn the Study Group Chairmen should sound out their members.

#### EC20/5 - The Universal Virus Database

- MCH - There are three databases in existence: (1) A highly structured custom-built Daisy database under development in Munich by Eichhorn with WHO support; (2) the database which will be demonstrated by AJDP employing Superbase 4 software and Windows 3 graphic interface for use on an IBM PC with mouse support; and (3) the interactive system being developed by AJG using Delta software (designed for taxonomy) also for use on an IBM PC.

The Eichhorn/WHO system has lengthy access times and is error-prone. At present it has 176 entries only, all from animal virology. It is not mouse driven. It is complex and not as intuitive as the AJDP/Superbase 4 system. It is inflexible and not user-friendly. Further development of this system is in doubt.

The AJDP/Superbase 4 system includes all the viruses listed in the current Arbovirus catalogue and the last ICTV Report; but it has to be revised and updated. This system is simple to use, expandable, and capacity is limited only by hard disc size. It is flexible and has extensive search facilities.

The Delta/AJG system contains some 400 entries, all plant viruses, and it is planned to increase the number of entries to 1200 by 1992. It is not user friendly in its present state of development.

To evaluate these systems we need to identify potential users and uses of a universal virus database, we need to consider also questions of ownership, copyright and revenue.

- AJG - The Delta system has been developed specifically for taxonomic purposes, with support from the Australian government which will end in 1992. The basic information for inclusion in the database is obtained by questionnaire designed to obtain diagnostic-type information. The information is stored as character and state, i.e. in numerical form not in words, hence the output can be modified (e.g. in different languages). So far it has been used to produce several books complete with identification keys, formatted straight from the computer (copies of these books were circulated for inspection). The output can also be obtained in microfiche form. A new version with Interkey format is being developed which will be mouse-driven and have greater search facilities than an ordinary database. Full colour photographs can be accommodated (2,500 per single CD ROM). It is intended to distribute the software and database as a CD or several discs; about 20 Mbyte required.

- FAM - What about ownership of this system?  
 AJG - Vague, still to be clarified.  
 MCH - Raw data are in the public domain, only the formatting can be patented.  
 CF - What are the plans for this system beyond 1992?  
 AJG - Probably will continue to maintain and develop it personally through CAB International.  
 AJDP - Our aim has been to develop a low cost system for use by a wide range of virologists. It employs Superbase 4 software and can be entered into any Windows program. It has been developed in house without direct support. Data were gathered from existing sources (ICTV and the Arbovirus Catalogue). It could be marketed at around \$100/copy and serviced by up-dates at \$50/copy. The Superbase 4 software is included, but the Windows 3 program is needed to operate it. It has digitised pictures in the database in monochrome (but colour could be added). Approximately 0.5 Mbyte would be required for one colour picture. This database is designed as a searchable information store, not for taxonomy. It is limited to use on an IBM PC, and it is unlikely that an Apple/Mac version could be produced. Anyone with Superbase 4 software can put information into the database; e.g. Study Groups could assist updating the database by inputting data directly.

(The system was demonstrated by AJDP and a demonstration disc was distributed).

- CF - Can data be transferred between this system and the Delta system and vice versa?  
 AJDP/AJG - Should be possible to write an appropriate program.  
 MCH - Are the literature references in a full form suitable for inclusion in publications?  
 AJDP/AJG - No.  
 FAM - Both systems have their strengths. The role of ICTV should be to support development of a single central database in order to attract the considerable financial support which will be required. What are the estimated costs of further development; what would \$100,000 provide?  
 AJG - Has required 4-5 man/years to develop the system to the present stage, and many man/years of effort to obtain and process the data. Much more than \$100k would be required to expand the system.  
 AJDP - \$100K would go some way to assist further development, but the Sub-committee would have to determine priorities.  
 DJM - How do you integrate molecular information into these two systems.  
 AJG - Genome maps could be included; anything more is already catered for by GenBank.  
 MHVR - The ICTV Report stops at the species level, the database to be useful should contain a detailed description of each species.  
 FAM - The input information should come from official sources to ensure reliability.  
 AJG - The Delta system is superior for taxonomy, but the use of Interkey requires a lot of knowledge. User-friendly software has still to be developed. Perhaps there is room for two systems. The immediate priority is to determine what information is required. An agreed set of descriptors is required. We also have to decide whether the output should be in book form or as provision of a central database. There is also the question of funding.  
 FAM - At Berlin the Bergey Trust expressed interest. Tomorrow we will consider these topics in more detail. There will be an open session with presentations from the observers, followed by a closed session. The database is the biggest task facing the ICTV in the next few years.  
 MHVR - We should be ready to instruct Study Group Chairmen to prepare lists of descriptors.

#### EC20/5 - The Universal Virus Database (Contd) - Open Session. Wednesday 24th April 1991.

- FAM - I now invite Dr. M.I. Krichevsky from NIH to open our discussion of this important topic.  
 MIK - There are various microbiological databases in existence, but none can be considered universal. Most are private, not shared; e.g. in hospitals, NIH, etc for logging of strains. There is an open database for the genus *Mycobacterium*, used for diagnostic purposes. There is also a database for hybridomas.

There are several reasons for the dearth of databases in microbiology; one is the question of what information to include - only 10% of any database is ever used. The users of databases are not specialists, i.e. there is a communication problem (e.g. immunologists do not make use of the hybridoma database because they are already aware of the information). Bergey's Manual is a database in printed form (incredibly the tapes were destroyed by the publisher after publication). There is also an arbovirus database already in existence, prepared at the Indian Institute of Virology in Pune.

The information encoded should begin from the lowest level achievable, e.g. the mean of a set of observations gives no information about the distribution if the primary data are missing. Therefore it is essential to start from the strain level; a structure can be built up from the primary level only, it is impossible to go backwards. There are now some 12,000 descriptors for bacteria, fungi and protozoa; any system must be open-ended. A common format must be adopted. Many early hospital databases have unique formats and the information contained is locked in that system. A basic format is required which can be processed in different ways. A quasi-binary system based on yes/no/don't know is optimal. Programmes have been developed to handle this type of coding. Another possibility is the Paradox Program.

An adequate source of long-term funding is a critical requirement. In the UK a Culture Collection Database was set up with government support. Funding ran out and the Database had to be transferred to Germany and UK users now have to pay to access information. The lack of long-term funding in this case means that the database is maintained but not up-dated and its usefulness will gradually erode.

Accessibility must also be considered. An enzyme nomenclature database has been developed, but is not accessible because book sales are used by the publisher to fund maintenance of the database.

The purpose and use of the database must be defined at the outset. It is important to design a coding system which can be used in different ways and does not limit further use. The important points are that the system must be built from the bottom up so that any hierarchal system can be accommodated, and it must have a mapping capability so that the content can be translated between systems. Binary coding can be mapped to the Delta system without difficulty. Binary coding compresses data; it takes more paper in the first instance, but processing and recall are faster.

Another consideration is that the database should be capable of being used for purposes other than taxonomy.

- FAM - Virology is in a transitional state; characterisation of viruses by serology is being superseded by PCR. Can a database cope with this? Bergey's Manual is out-of-date before it is published. Virology moves even faster.
- MIK - The technology can cope with this. There is a trend towards lower costs in package switching, academic networks can be used, and wide band systems are increasing speeds.
- AJG - No academic database can be self-supporting. The costs of building the database cannot be recovered; hardcopy is what makes the money.
- FAM - Should ICTV be part of an international effort with a commitment from WHO, FAO, etc to maintain the database?
- BWJM - Should this effort be under the ICSU Codata umbrella?
- MIK - The ICSU/Codata microbial strain database only recovers 20% of its costs, because there are only about 400 users and the fees are too low.
- DJM - The question of magnitude is relevant. The specific requirements of ICTV are less than those of a comprehensive database.
- MIK - Bergey's Manual is published in a 12 year cycle. Their requirement for a database is speed of production not of provision of a database as such. This affects the overall cost. Perhaps the ICTV should approach sponsors with a specific proposition, with the generation of a universal database as a spin-off. It is important to keep the system open-ended. Drawing up a character list is the most important step; everything should be included.
- JM - A problem with the latter is that the quality of the information is variable. E.g. the estimation of bacterial genome size by older techniques is grossly inaccurate. Should older data be excluded?

- MIK - It is like reading the scientific literature; the axiom is "reader beware". It is a value judgement, but it should be amenable to evaluation by sorting (e.g. by date, method, etc). Everything should be included, logging into the database is only 5% of the cost of acquiring the data. Most data are one-off observations, furthermore there is a 1-2% error in recording of original data. It is an assumption that most, but not all, of the information in a database is reliable.
- FAM - Thank you. Lois Blaine (Bioinformatics Department, ATCC) will now tell us about the ATCC involvement.
- LB - ATCC does not want to build a separate database. The Delta system has been installed for plant viruses and the RCK system for bacteria, but there is no animal virus database. The Atherton and Pune systems have been examined, and we are involved in the Codata STABD (Standard Terminology Access to Biological Data) project. NSF has been approached for funding, and a meeting to examine the database question was held in 1990. (The report of this meeting was circulated). The conclusions were that (1) databases are not established for historical purposes, therefore outmoded data should be filtered out; (2) the content can only be determined by local subjective judgement - e.g. incorporation of strain variation might be important in the case of HIV, but not in other cases because the information is just not available. The ICTV should provide a blue-print for establishing a database. The objectives of the database should include a facility to provide data for reports, to be universal and compatible with different types of computer, have graphics capability, and have both commercial and academic interest. The hardware is well-ahead of the software and the human ability to use it, the limiting factor is financial resources.

The NSF Workshop formulated a list of conclusions (distributed by LB): (1) It would not be difficult to merge animal and plant virus data. Funding has been requested from NSF (decision in June) for a person (2/3rds salary for 2 years) to compile a common list of descriptors. This list would be circulated to ICTV Study Groups and appraised by the Executive Committee. (A preliminary list of descriptors was circulated). (2) The advantages and disadvantages of a standardised set of descriptors were identified.

A stable financial base is required, because it is a slow process and volunteer dependent. ICTV could provide the organisation.

- FAM - Modules already exist; the Arbovirus Catalogue is maintained by CDC, there is a market for the plant virus database, only the bacterial viruses lack support.
- LB - Point (3), (4) and (5) concerned production of a unified system of descriptors and has already been discussed. Point (6) suggested that ICTV should take the lead, and points (7) and (8) concerned implementation of the proposals.
- FAM - It is unfortunate that neither ICTV nor IUMS were invited to or aware of this meeting.
- LB - This was one of the unfortunate consequences of the illness and death of Richard Francki. The grant proposal was presented to NSF with the support of AJG. ATCC will not benefit financially.
- FAM - Your invitation to become a member of the ICTV Database Sub-committee should restore the situation.
- MIK - The ICTV should copyright the approved list of descriptors as soon as it is prepared and then proceed from there. This will give legal backing to ICTV's function. The list can be copyrighted, because Karger have copyright of the format only not the content.
- FAM - I propose that AJG should provide examples of lists of descriptors to the Executive Committee before the next meeting. (EC20/6/1). Sub-committees will need to bring their terminologies into line.
- MHVR - The ICTV should accept full responsibility for compiling the lists and not consult other interested parties (e.g., NIH, WHO, etc), because of the time delay.
- MIK - You could send first drafts to others for comments, but still retain editorial decision.
- MAM - Who will monitor the database for errors?
- AJG - The data are checked and the entries are up-dated where information is made available. This is a problem because people are reluctant to go back over old data.
- MIK - There is another inherent problem: e.g. an error is detected in a Table in a paper - do you correct the Table and retain the uncorrected reference without a foot-note.

- LB - The database is an advance on conventional literature searches and abstract lists, because it is possible to have a rolling correction facility.
- FAM - What happens when you leave ATCC?
- LB - My role is finished and AJG will have to assume the role of coordinator.
- CHC - We must give thought to identifying potential users and defining the purposes of the database.
- CRP - Potential users include international organisations (WHO, FAO, UNESCO, etc), national laboratories (NIH, CDC, etc), government agencies (NSF, National Research Councils, EEC, etc), academic and industry research institutes, hospitals, universities, academic teachers and students, publishers, libraries, the media, and of course taxonomists. The system given ICTV blessing must be flexible enough to accommodate the needs of these diverse users. We must seek to service the widest potential market. The Delta system seems to me to have the greater power and the greater facility to handle the type of data we will be providing. On the other hand the Superbase 4 system has the advantage of simplicity.
- CF - Do we need to make a decision on the type of software now?
- AJG - There is a need to establish a primary data set immediately which can be processed subsequently in Delta and Superbase format, and used for different end products, i.e. books, ICTV Reports, etc. We need to begin collecting primary data as soon as possible.
- MIK - There is a need to refine the logging of the primary data set; it should be maintained in a form which can be used in different languages.
- CF - The EEC are interested in providing support for a database, but have not yet identified the appropriate organisation to support. ICTV must present its case as soon as possible. The EEC will support a collaborative international effort, provided the product will be made available in Europe, and there is a European participant.
- FAM - Regarding implementation, there are only 18 months left for preparation of the Sixth Report. Our target should be to produce the Seventh Report in database form. What is the interest in the two current databases?
- AJDP - There has been some interest in the Superbase 4 system because of its user friendliness. A niche market already exists.
- AJG - In terms of book production, use of the Delta database has been encouraging.
- LB - Like apple-pie and motherhood, everyone wants a database but no-one is prepared to pay for information. Without a market the project will wither. The dilemma is that the database has to be created and demonstrated to seek out customers.
- FAM - Sale of the ICTV 5th Report will indicate the size of the potential market (Springer is expecting up to 4,000 sales).
- AJDP - The Superbase 4 system could be updated to include all the data contained in the 5th Report within six months. It could be expanded subsequently when the primary data is collected.
- LB - We are on the right track now. ICTV could promote both the Delta and Superbase systems. AJG should prepare a paper outlining the present situation, the action being taken, and the future prospects.
- AJG - A first draft of the list of descriptors could be prepared for distribution to Study Groups within 3-4 months.
- MIK - There are no conceptual problems to be overcome. The main hurdles are organisational and marketing.

EC20/5 (Contd.) - The Universal virus Database - Closed Session, Wednesday 24th April, 1991.

- FAM - I think it can be assumed that the ICTV has recaptured the lead in this area. The Virus Database Sub-committee has an enormous load; the full cooperation of Sub-committee chairmen is essential. I thank AJG for taking on this role. If funding can be obtained it would be appropriate to include a vertebrate virologist in the project. Maybe CF could ascertain if the EEC would support someone to spend a sabbatical year with AJG?

- CF - It should be formally recorded at this juncture that it was agreed that "The ICTV will take responsibility for establishment of a universal virus database". (EC20/6/2).
- DJM - There will be organisational problems; perhaps the Sub-committee structure is not appropriate for this task. A principal investigator should be identified to be the focus for research funding. The ICTV would need to take responsibility for purchase and ownership of equipment. There is also the issue of training and continuity. A host institution should be identified to allow capital investment and facilitate international money transfer. A long term stable background is essential.
- AJG - The database should be portable. Both the Delta and Superbase 4 systems are PC-based and easily transferable.
- CF - The EEC has substantial financial support available for this purpose, and would support an Australian based operation provided there was a European component. The timetable of the EEC programme is already fixed; it would be sufficient to have a draft application ready for approval at the next Executive Committee meeting.
- MHVR - The application for funding should be made through the Virology Division of IUMS, indicating support from Codata (Lois Blaine).
- MAM - We need to have a policy on distribution, copyright, etc., and the use of the existing plant virus database.
- CF - We have to decide whether we are aiming for public support to develop a commercial database, or to establish a service entirely supported by public funds.
- FAM - It should be saleable. It is accepted practice, in the USA, at least for donors to buy and donate such material to those who cannot afford to purchase it.
- GPM - Even so it is difficult to see that the yield would be sufficient to maintain the database. The more we charge, the more restricted will be the use.
- AJDP - The primary database provided it is not confined to one site could be up-dated directly from the Study Groups. If chairmen were trained to be able to enter data the costs of maintaining the database might not be so great.
- MHVR - There is the problem of continuity. There are 39 Study Groups with rolling membership. It would be difficult to maintain a steady flow of data; *de facto* only very few chairmen would be effective in this role and there would have to be some mechanism for retaining them.
- MAM - What is the precise role of the Study Groups. Are they set up to address problem areas, and are they appropriate to this task?
- HGP - Historically the Study Groups were created to represent the whole virus community and to act as a counterweight to the Executive Committee.
- FAM - Maybe there is now a need for nominated members. This is a subject for the next agenda. At present the ICTV Study Groups have a narrow national/gender/subject basis and the formation of more Study Groups should be encouraged. For other reasons it might be advantageous to have a Japanese member of the Executive Committee.
- AJG - To return to the question of funding, an open public system is out because the product is a book in the case of the Delta system. We do need to recover the costs plus some surplus in order to maintain and develop the system.
- FAM - I think that this is the consensus opinion and that we should give FC/CRP authority to negotiate according to circumstance.
- SAG - Can the Fifth Report be published in Superbase 4 format?
- AJDP - The Format of the Report is copyrighted, but we can extract all the relevant data. If we go along that path we need to be sure that we will cover our costs.
- AJG - If we could put it into Delta format and write a program to convert it to Superbase 4 we would kill two birds with one stone.
- MHVR - The international copyright implications should be clarified. (An international patent lawyer could be consulted to obtain an informed opinion).
- AJDP - Cost of producing a Superbase 4 copy would be about \$30 per copy. The endorsement of the Executive Committee would be required before release.
- FAM - Preparation should go ahead, pending clarification of the copyright situation. Copies could be offered at \$60-100 each. The potential market could be assessed by advertising for subscriptions in Archives, a stand at the ASM, etc.
- AWJ - This would also reinforce the message that ICTV is now taking a lead in the business of electronic publishing.



- MAM** - A final item. The Executive Committee should provide some guidance on the naming of viruses and groups. A few names have been bounced recently and some very poor names adopted. If we are intending to proceed to binominal names, shorter and more euphonic designations are required. Maybe this item should be placed on the agenda for the next meeting.
- CHC** - The Executive Committee should revise its procedures in this respect. Recently names have been imposed from above without consultation with or even notification of Study Groups.

A list of deadlines and responsibilities extracted from the hand-written minutes was compiled and circulated by CRP. The meeting adjourned at 3.55 p.m. The location and date of the next meeting will be decided within the next four weeks and information circulated as soon as possible.

## APPENDIX

### SUMMARY OF DECISIONS, DELEGATED RESPONSIBILITIES AND DEADLINES.

#### Implemented decisions:

- EC20/2/1 - The Summary Tables in the Fifth Report will be changed to read Genus/Group instead of Family/Group.
- EC20/2/5 - Following an intervention by DHLB and in line with a decision at a previous meeting the President decided that from the Sixth Report onwards all members of Study Groups would be listed as authors of family descriptions.
- EC20/2/7 - *Badnavirus* was adopted as a group name.
- EC20/4/1 - The species concept as elaborated by MHVR should be accepted by the ICTV forthwith.
- EC20/4/2 - The definition of species approved for inclusion in the Sixth Report to replace rule 10 is that: "A virus species is a polythetic class of viruses that constitutes a replicating lineage and occupies a particular ecological niche".
- EC20/6/2 - The ICTV will take responsibility for establishment of a universal virus database.

#### Decisions still to be implemented with approximate deadlines for action:

- EC20/2/2 - A set of guide-lines will be prepared by FAM and CF for distribution to Sub-committee and Study Group chairmen prior to revision of descriptions for the Sixth Report.  
Deadline: As soon as possible
- E20/2/3 - Sub-committee Chairmen will circulate the guide-lines and template as soon as available to Study Group Chairmen.  
Deadline: As soon as possible
- EC20/2/4 - A Sub-committee comprising HWA, CHC, LB (Chairman), and RG will consider revision of the line diagrams and illustrations for the Sixth Report.  
Deadline: Before April 1992.
- EC20/2/6 - Acronyms in common usage will be included in the Sixth Report. DHLB will be responsible for preparation of a list of acronyms of vertebrate viruses.  
Deadline: End of January 1992.
- EC20/2/8 - Each Sub-committee chairman will prepare a list of unclassified agents for consideration at the next meeting.  
Deadline: End of January 1992.
- EC20/2/9 - An ad hoc Study Group on satellites will be set up by MAM.  
Deadline: As soon as convenient.
- EC20/3/1 - JHS and DJM were invited to consider the issue of higher taxa further and to be prepared to continue the discussion at the next meeting.  
Deadline: Before April 1992.
- EC20/3/2 - A position paper on the issue of higher taxa will be prepared by JHS, DJM, KWB and FAM for inclusion in Virology Division News.  
Deadline: As soon as possible

- EC20/3/3** - A sub-committee comprising RG (chairman), JHS, DJM and MHVR is invited to consider the preparation and format of an Executive Committee Report to supplement or replace the President's Report in the Sixth Report.  
Deadline: Before April 1992.
- EC20/4/3** - A sub-committee of CHC, JM and MHVR will prepare definitions of the terms polythetic class, replicative lineage and ecological niche, and report their decisions to ICTV within three months.  
Deadline: Before September 1991.
- EC20/4/4** - Sub-committee chairmen should now instruct Study Group Chairmen to delineate species, and the Executive Committee should produce a guidance document. (None of the properties need imply a hierarchy and Study Groups should not search for such).  
Deadline: As soon as possible
- EC20/4/5** - AJG and HGP are invited to prepare a background paper and proposal on the question of the incorporation of the genus name into the virus designation for the next meeting.  
Deadline: By January 1992.
- EC20/4/6** - JM will send a letter to Sub-committee and Study Group chairmen requesting information on how Study Groups operate and reach their decisions. The results of this survey should be circulated to the Executive Committee before the next meeting.  
Deadline: By January 1992.
- EC20/6/1** - AJG is invited to prepare representative lists of descriptors for consideration by the Executive Committee before the next meeting.  
Deadline: Before April 1992.